

1652

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/492,029

DATE: 12/07/2000
TIME: 10:22:40

Does Not Comply
Corrected Diskette Needed

Input Set : A:\-927-1.app
Output Set: N:\CRF3\12072000\I492029.raw

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3 <110> APPLICANT: Zuker, Charles S.
4     Adler, Jon Elliot
5     Lindemeier, Juergen
6     The Regents of the University of California
8 <120> TITLE OF INVENTION: Assays for Sensory Modulators Using a Sensory Cell
9     Specific G-Protein Beta Subunit
11 <130> FILE REFERENCE: 02307E-092710US
13 <140> CURRENT APPLICATION NUMBER: US 09/492,029
14 <141> CURRENT FILING DATE: 2000-01-26
16 <150> PRIOR APPLICATION NUMBER: US 60/117,404
17 <151> PRIOR FILING DATE: 1999-01-27
19 <160> NUMBER OF SEQ ID NOS: 5
21 <170> SOFTWARE: PatentIn Ver. 2.1
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24 <211> LENGTH: 156
25 <212> TYPE: DNA
26 <213> ORGANISM: Rattus sp.
28 <220> FEATURE:
29 <223> OTHER INFORMATION: rat tongue circumvallate papillae taste receptor
30     cell cDNA clone 165-17
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33 aacaaaaggg cataaagaaa gtggctggga gggagccagg atactaggag tgacacctat 60
34 agtcatgggc tgagcgctct gccattccc argccggaca aaggctgctg gtageccagg 120
35 agtcatctag ggtggggagg gtcgtttctt gtttat 156
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44 <221> NAME/KEY: CDS
45 W--> <222> LOCATION: (78). (1097) (2000)
46 <223> OTHER INFORMATION: rat taste cell specific G-protein beta 3 subunit
47     (TC-Gbeta3)
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52 cccttgacct gtgaacc atg ggg gag atg gag cag ctg aag cag gag gcg 110
53     Met Gly Glu Met Glu Gln Leu Lys Gln Glu Ala 10
54     1 5
56 gag cag ctc aag aag cag att gct gat gcc agg aaa gcc tgt gcg gac 158
57 Glu Gln Leu Lys Lys Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp 25
58     15 20
60 atc act ctg gct gag ctt gtg tct ggc ctg gag gtg gtg gga cga gtc 206
61 Ile Thr Leu Ala Glu Leu Val Ser Gly Leu Glu Val Val Gly Arg Val 40
62     30 35
64 cag atg cgg aca cgg aag acg lta agg gga cac ctg gct aag atc tat 254
65 Gln Met Arg Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr 55
66     45 50

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68 gcc atg cac tgg gcc act qac tct aag ctg cta gta agt gcc tcg cag 302
69 Ala Met His Prp Ala Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln
70 60 65 70 75
72 gat ggg aag ctg atc gtg tgg qac act tac acc aat aag gtg cat 350
73 Asp Gly Lys Leu Ile Val Trp Asp Thr Tyr Thr Thr Asn Lys Val His
74 80 85 90
76 gct atc ccg ctg cgt tcc tcc tgg gtc atg acc tgt gcc tat qca cca 398
77 Ala Ile Pro Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro
78 95 100 105
80 tca ggg aac ttc gtg gca tgt ggg ggg cta gat aac atg tgc tca atc 446
81 Ser Gly Asn Phe Val Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile
82 110 115 120
84 tac agc ctc aaa tcc cgt gag ggc aat gtc aag gtc agc cgg gaa ctc 494
85 Tyr Ser Leu Lys Ser Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu
86 125 130 135
88 tcg gct cac aca ggt tat ctc tcc tgt tgc cgc ttc ctg gat qac aac 542
89 Ser Ala His Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn
90 140 145 150 155
92 aac att gtg act agc tct ggg gac acc acg tgt gcc ttg tgg gac att 590
93 Asn Ile Val Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile
94 160 165 170
96 gag acg ggg cag cag aag aca gtg ttc gtg gga cac act ggt gac tgc 638
97 Glu Thr Gly Gln Gln Lys Thr Val Phe Val Gly His Thr Gly Asp Cys
98 175 180 185
100 atg aac ctg gct gtg tcc cca qac tac aaa ctc ttc atc tcg gga gct 686
101 Met Ser Leu Ala Val Ser Pro Asp Tyr Lys Leu Phe Ile Ser Gly Ala
102 190 195 200
104 tgt gat gcc agc gcc aag ctc tgg gat gtg agg gaa ggg acc tgt cgc 734
105 Cys Asp Ala Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg
106 205 210 215
108 cag act ttc act ggc cac gag tca gac atc aat gct atc tgt ttc ttt 782
109 Glu Thr Phe Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe
110 220 225 230 235
112 ccc aat ggg gag gcc atc tgc act ggc tca gat gat gcc tcc tgc cgc 830
113 Pro Asn Gly Glu Ala Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg
114 240 245 250
116 ctc ttt gac ctg agg gca gac cag gaa ctg aca gcc tac tcc cac gag 878
117 Leu Phe Asp Leu Arg Ala Asp Gln Glu Leu Thr Ala Tyr Ser His Glu
118 255 260 265
120 agc atc atc tgt ggc atc acg tcc gta gcc ttc tca ctc agt ggt cgc 926
121 Ser Ile Ile Cys Gly Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg
122 270 275 280
124 ctg ctc ttt gct ggc tat gat gac ttc aac tgc aat gtc tgg gac tct 974
125 Leu Leu Phe Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser
126 285 290 295
128 ctg aag tgt gag cgt gta ggc gtt ctt tct ggc cat gac aac aga gtc 1022
129 Leu Lys Cys Glu Arg Val Gly Val Leu Ser Gly His Asp Asn Arg Val
130 300 305 310 315
132 agt tgc ctg ggg gtc aca gct gac ggc atg gct gtg gcc act gga tcc 1070

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133 Ser Cys Leu Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser
134                               320           325           330           1117
136 tgg gac agc ttc ctc aaq atc tgg aac tgaggaggct ggagggaagag
W--> 137 Trp Asp Ser Phe Leu Lys Ile Trp Asn
138                               335           340
140 glgggaagcc atgaaggctc tcagctgact cctatgccct gtctccttag ggtcagtttt 1177
142 ctataccctg ggccactcc cagtaaaactt ccttctaagg gcaagtgagg tlataggaqt 1237
144 gtgccttttg gaggtagcag gtcacaaggg caaagaactg cccattttcc tccagggcct 1297
146 ctctctccca cagtcctcat agcttctccc ttcataaaca agaacagacc cccccaccc 1357
148 tagatgactc ctgggctacc agcagcggtt gtccggcctg ggaatggcca gagcgctcag 1417
150 cccatgacta taggigtcac tcctagtalc ctggctccct cccagcgact tctttctgc 1477
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155 <210> SEQ ID NO: 3
156 <211> LENGTH: 340
157 <212> TYPE: PRT
158 <213> ORGANISM: Rattus sp.
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164 Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Ile Thr Leu Ala Glu
165 20 25 30
167 Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg Thr Arg
168 35 40 45
170 Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala
171 50 55 60
173 Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
174 65 70 75 80
176 Val Trp Asp Thr Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg
177 85 90 95
179 Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val
180 100 105 110
182 Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Ser Leu Lys Ser
183 115 120 125
185 Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly
186 130 135 140
188 Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Ile Val Thr Ser
189 145 150 155 160
191 Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
192 165 170 175
194 Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
195 180 185 190
197 Ser Pro Asp Tyr Lys Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
198 195 200 205
200 Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
201 210 215 220
203 His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly Glu Ala
204 225 230 235 240
206 Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp Leu Arg
207 245 250 255

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209 Ala Asp Gln Glu Leu Thr Ala Tyr Ser His Glu Ser Ile Ile Cys Gly
210                               260                               265                               270
212 Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe Ala Gly
213                               275                               280                               285
215 Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Leu Lys Cys Glu Arg
216                               290                               295                               300
218 Val Gly Val Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu Gly Val
219 305                               310                               315                               320
221 Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu
222                               325                               330                               335
224 Lys Ile Trp Asn
225                               340
229 <210> SEQ ID NO: 4
230 <211> LENGTH: 1523
231 <212> TYPE: DNA
232 <213> ORGANISM: Homo sapiens
234 <220> FEATURE:
235 <221> NAME/KEY: CDS
236 <222> LOCATION: (7)..(1029)
237 <223> OTHER INFORMATION: human taste cell specific G-protein beta 3 subunit
239 <400> SEQUENCE: 4
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242 1 5 10
244 aag aag cag att gca gat gcc agc aaa gcc tgt gct gac gtt act ctg 96
245 Lys Lys Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu
246 15 20 25
248 gca gag ctg gtg tct ggc cta gag gtg gtg gga cga gtc cag atg cgg 144
249 Ala Glu Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg
250 35 40 45
252 acg cgg cgg acg tta agc gga cac ctg gcc aag att tac gcc atg cac 192
253 Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His
254 50 55 60
256 tgg gcc act gat tct aag ctg ctg gta agt gcc tcg caa gat ggg aag 240
257 Trp Ala Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Glu Asp Gly Lys
258 65 70 75
260 ctg atc gtg tgg gac agc tac acc acc aac aag gtg cac gcc atc cca 288
261 Leu Ile Val Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro
262 80 85 90
264 ctg cgc tcc tcc tgg gtc atg acc tgt gcc tat gcc cca tca ggg aac 336
265 Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn
266 95 100 105
268 ttt gtg gca tgt ggg ggg ctg gac aac atg tgt tcc atc tac aac ctc 384
269 Phe Val Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu
270 115 120 125
272 aaa tcc cgt gag ggc aat gtc aag gtc agc cgg gag ctt tct gct cac 432
273 Lys Ser Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His
274 130 135 140
276 aca ggt tat ctc tcc tgc tgc cgc ttc ctg gat gac aac aat att gtg 480

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277 Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val
278 145 150 155 528
280 acc aqc tgc ggc gac acc acg tgt gcc ttg tgg gac att gag act ggg
281 Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly
282 160 165 170 576
284 cag cag aag act gta ttt gtg gga cac acg ggt gac tgc atg agc ctg
285 Gln Gln Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu
286 175 180 185 190 624
288 gct gtg tct cct gac ttc aat ctc ttc att tcg ggg gcc tgt gat gcc
289 Ala Val Ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala
290 195 200 205 672
292 agt gcc aag ctc tgg gat gtg cga gag ggg acc tgc cgt cag act ttc
293 Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe
294 210 215 220 720
296 act ggc cac gag tgc gac atc aac gcc atc tgt ttc ttc ccc aat gga
297 Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly
298 225 230 235 768
300 gag gcc atc tgc acg ggc tgc gat gac gct tcc tgc cgc ttg ttt gac
301 Glu Ala Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp
302 240 245 250 816
304 ctg cgg gca gac cag gag ctg atc tgc ttc tcc cac gag agc atc atc
305 Leu Arg Ala Asp Gln Glu Leu Ile Cys Phe Ser His Glu Ser Ile Ile
306 255 260 265 270 864
308 tgc ggc atc acg tcc gtg gcc ttc tcc ctc agt ggc cgc cta cta ttc
309 Cys Gly Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Phe
310 275 280 285 912
312 gct gac tac gac gac ttc aac tgc aat gtc tgg gac tcc atg aag tct
313 Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Met Lys Ser
314 290 295 300 960
316 gag cgt gtg ggc atc ctc tct ggc cac gat aac agg gtg agc tgc ctg
317 Glu Arg Val Gly Ile Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu
318 305 310 315 1008
320 gga gtc aca gct gac ggg atg gct gtg gcc aca ggt tcc tgg gac agc
321 Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser
322 320 325 330 1056
324 ttc ctc aaa atc tgg aac tgaggaggt ggagaaagg aagtggagg
325 Phe Leu Lys Ile Trp Asn
326 335 340
328 cagtgaacac actcagcagc cccctgcccg accccatctc attcaggtgt tctcttctat 1116
330 attccgggtg ccattccac taagctttct cctttgaggg cagtggggag catgggactg 1176
332 tgcctttggg aggcagcatc agggacacag gggcaaaagaa ctgcccacac tccctccatg 1236
334 gccttccctc cccacagtc tccagcctc tcccttaatg agcaaaggaca acctgccctc 1296
336 cccagccctc ttgcagggcc agcagacttg agtctgaggc cccagggcct aggtattcctc 1356
338 cccagagccc actaccttg tccaggcctg ggtggtatag ggcgtttggc cctgtgacta 1416
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345 <210> SEQ ID NO: 5
346 <211> LENGTH: 340
347 <212> TYPE: PRT

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12/7/00

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/492,029

DATE: 12/07/2000
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Input Set : A:\-927-1.app
Output Set: N:\CRF3\12072000\I492029.raw

L:45 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:2, CDS LOCATION: (78)..(2000)
L:137 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 2, CDS LOCATION:78..2000